

WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising
 - a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,
 - 5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,
 - a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,
 - a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,
 - 10 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,
 - a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,
 - 15 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,
 - a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,
 - a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,
 - 20 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,
 - a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
 - 25 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
 - a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
 - wherein the nucleic acid encodes a fluorescent polypeptide and the
 - 30 sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.
2. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 200 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 200 residues,
- 5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 200 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 200 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 200 residues,
- 10 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 200 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 200 residues,
- 15 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 200 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 200 residues,
- a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 200 residues,
- 20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 200 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 200 residues, or
- 25 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 200 residues.

3. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

- 30 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 300 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 300 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 300 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 300 residues,

5 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 300 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 300 residues,

10 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 300 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 300 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 300 residues,

15 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 300 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 300 residues,

20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 300 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 300 residues.

25 4. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 400 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 400 residues,

30 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 400 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 400 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 400 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 400 residues,

5 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 400 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 400 residues,

10 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 400 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 400 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 400 residues,

15 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 400 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 400 residues.

20 5. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 500 residues,

25 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 500 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 500 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 500 residues,

30 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 500 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 500 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 500 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 500 residues,

5 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 500 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 500 residues,

10 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 500 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 500 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 500 residues.

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6. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 600 residues,

20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 600 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 600 residues,

25 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 600 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 600 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 600 residues,

30 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 600 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 600 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 600 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 600 residues,

5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 600 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 600 residues, or

10 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 600 residues.

7. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

15 a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

20 a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

25 a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

30 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

5 a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues.

8. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises:

10 a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

15 a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

25 a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

30 a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues.

5 9. The isolated or recombinant nucleic acid of claim 8, wherein the nucleic acid comprises

a nucleic acid sequence having at least 98% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 98% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

10 a nucleic acid sequence having at least 98% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 98% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

15 a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

25 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 98% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 98% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

30 a nucleic acid sequence having at least 98% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues.

10. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

a nucleic acid sequence having at least 99% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 99% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

5 a nucleic acid sequence having at least 99% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 99% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

10 a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

15 a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

20 a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 99% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 99% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

25 a nucleic acid sequence having at least 99% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues.

11. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises

30 a nucleic acid having a sequence as set forth in SEQ ID NO:1,
a nucleic acid having a sequence as set forth in SEQ ID NO:3,
a nucleic acid having a sequence as set forth in SEQ ID NO:5,
a nucleic acid having a sequence as set forth in SEQ ID NO:7,
a nucleic acid having a sequence as set forth in SEQ ID NO:9,

a nucleic acid having a sequence as set forth in SEQ ID NO:11,
a nucleic acid having a sequence as set forth in SEQ ID NO:13,
a nucleic acid having a sequence as set forth in SEQ ID NO:15,
a nucleic acid having a sequence as set forth in SEQ ID NO:17,
5 a nucleic acid having a sequence as set forth in SEQ ID NO:19,
a nucleic acid having a sequence as set forth in SEQ ID NO:21,
a nucleic acid having a sequence as set forth in SEQ ID NO:23, or
a nucleic acid having a sequence as set forth in SEQ ID NO:25.

10 12. The isolated or recombinant nucleic acid of claim 1, wherein the
nucleic acid sequence encodes a polypeptide comprising

a polypeptide having a sequence as set forth in SEQ ID NO:2,
a polypeptide having a sequence as set forth in SEQ ID NO:4
a polypeptide having a sequence as set forth in SEQ ID NO:6,
15 a polypeptide having a sequence as set forth in SEQ ID NO:8,
a polypeptide having a sequence as set forth in SEQ ID NO:10,
a polypeptide having a sequence as set forth in SEQ ID NO:12,
a polypeptide having a sequence as set forth in SEQ ID NO:14,
a polypeptide having a sequence as set forth in SEQ ID NO:16,
20 a polypeptide having a sequence as set forth in SEQ ID NO:18,
a polypeptide having a sequence as set forth in SEQ ID NO:20,
a polypeptide having a sequence as set forth in SEQ ID NO:22,
a polypeptide having a sequence as set forth in SEQ ID NO:24, or
a polypeptide having a sequence as set forth in SEQ ID NO:26.

25 13. The isolated or recombinant nucleic acid of claim 1, wherein the
sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering
setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to
default.

30 14. The isolated or recombinant nucleic acid of claim 1, wherein the
fluorescent polypeptide comprises a green fluorescent protein.

15. The isolated or recombinant nucleic acid of claim 1, wherein the fluorescent polypeptide comprises a cyan fluorescent protein.

5 16. The isolated or recombinant nucleic acid of claim 1, wherein a fluorescent activity comprises emission between about 500 nm (green) and 507 nm (green).

10 17. The isolated or recombinant nucleic acid of claim 1, wherein a fluorescent activity comprises emission between about 490 nm (cyan) and 491 nm (cyan).

18. The isolated or recombinant nucleic acid of claim 1, wherein the polypeptide comprises fluorescent activity after excitation at 485 nm (for green).

15 19. The isolated or recombinant nucleic acid of claim 1, wherein the polypeptide comprises fluorescent activity after excitation at 460 nm (for cyan).

20. The isolated or recombinant nucleic acid of claim 1, wherein the polypeptide retains a fluorescent activity under conditions comprising about pH 3.0.

20 21. The isolated or recombinant nucleic acid of claim 20, wherein the polypeptide retains a fluorescent activity under conditions comprising about pH 3.5.

25 22. The isolated or recombinant nucleic acid of claim 20, wherein the polypeptide retains a fluorescent activity under conditions comprising about pH 4.0.

23. The isolated or recombinant nucleic acid of claim 1, wherein the fluorescence is thermostable.

30 24. The isolated or recombinant nucleic acid of claim 23, wherein the polypeptide retains a fluorescent activity under conditions comprising a temperature range of between about 30°C to about 90°C.

25. The isolated or recombinant nucleic acid of claim 1, wherein the fluorescence is thermotolerant.

26. The isolated or recombinant nucleic acid of claim 25, wherein the polypeptide retains a fluorescent activity under conditions comprising a temperature range of between about 30°C to about 100°C.

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27. The isolated or recombinant nucleic acid of claim 1, wherein the polypeptide retains a fluorescent activity under conditions comprising treatment for a period up to about 50 hours with 6M guanidine HCL, 8M urea or 1% SDS.

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28. The isolated or recombinant nucleic acid of claim 1, wherein the polypeptide retains a fluorescent activity under conditions comprising treatment for a period up to about 50 hours with trypsin, chymotrypsin, papain, subtilisin, thermolisin, or pancreatin under conditions comprising a concentration range of up to about 1 mg/ml.

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29. An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a sequence comprising
a nucleic acid sequence as set forth in SEQ ID NO:1,
a nucleic acid sequence as set forth in SEQ ID NO:3,
a nucleic acid sequence as set forth in SEQ ID NO:5,
20 a nucleic acid sequence as set forth in SEQ ID NO:7,
a nucleic acid sequence as set forth in SEQ ID NO:9,
a nucleic acid sequence as set forth in SEQ ID NO:11,
a nucleic acid sequence as set forth in SEQ ID NO:13,
a nucleic acid sequence as set forth in SEQ ID NO:15,
25 a nucleic acid sequence as set forth in SEQ ID NO:17,
a nucleic acid sequence as set forth in SEQ ID NO:19,
a nucleic acid sequence as set forth in SEQ ID NO:21,
a nucleic acid sequence as set forth in SEQ ID NO:23, or
a nucleic acid sequence as set forth in SEQ ID NO:25,
30 wherein the nucleic acid encodes a fluorescent polypeptide.

30. The isolated or recombinant nucleic acid of claim 29, wherein the nucleic acid is at least about 100 residues in length.

31. The isolated or recombinant nucleic acid of claim 29, wherein the nucleic acid is at least about 200, 300, 400, 500, or 600 residues in length or the full length of the gene or transcript.

5 32. The isolated or recombinant nucleic acid of claim 29, wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

33. A nucleic acid probe for identifying a nucleic acid encoding a
10 fluorescent polypeptide, wherein the probe comprises at least 10 consecutive bases of a sequence comprising:

a sequence as set forth in SEQ ID NO:1,
a sequence as set forth in SEQ ID NO:3,
a sequence as set forth in SEQ ID NO:5,
15 a sequence as set forth in SEQ ID NO:7,
a sequence as set forth in SEQ ID NO:9,
a sequence as set forth in SEQ ID NO:11,
a sequence as set forth in SEQ ID NO:13,
a sequence as set forth in SEQ ID NO:15,
20 a sequence as set forth in SEQ ID NO:17,
a sequence as set forth in SEQ ID NO:19,
a sequence as set forth in SEQ ID NO:21,
a sequence as set forth in SEQ ID NO:23, or
a sequence as set forth in SEQ ID NO:25,
25 wherein the probe identifies the nucleic acid by binding or hybridization.

34. The nucleic acid probe of claim 33, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a sequence comprising:

30 a sequence as set forth in SEQ ID NO:1,
a sequence as set forth in SEQ ID NO:3,
a sequence as set forth in SEQ ID NO:5,
a sequence as set forth in SEQ ID NO:7,
a sequence as set forth in SEQ ID NO:9,

a sequence as set forth in SEQ ID NO:11,
 a sequence as set forth in SEQ ID NO:13,
 a sequence as set forth in SEQ ID NO:15,
 a sequence as set forth in SEQ ID NO:17,
 5 a sequence as set forth in SEQ ID NO:19,
 a sequence as set forth in SEQ ID NO:21,
 a sequence as set forth in SEQ ID NO:23, or
 a sequence as set forth in SEQ ID NO:25.

10 35. A nucleic acid probe for identifying a nucleic acid encoding a
 fluorescent polypeptide, wherein the probe comprises a nucleic acid sequence
 comprising:

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:1 over a region of at least about 100 residues,
 15 a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:3 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:5 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 20 NO:7 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 NO:9 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 25 NO:11 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 NO:13 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 70% sequence identity to SEQ ID
 NO:15 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 30 NO:17 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 70% sequence identity to SEQ ID
 NO:19 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

5 wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

36. The nucleic acid probe of claim 35, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70,
10 about 40 to 80, or about 60 to 100 consecutive bases of a nucleic acid sequence selected from the group consisting of a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a
15 subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof,
20 a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

37. The nucleic acid probe of claim 35, wherein the probe comprises a nucleic acid sequence having at least 90% sequence identity to a nucleic acid sequence
25 comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth
30 in SEQ ID NO:13, or a subsequence thereof; a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ

ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

38. The nucleic acid probe of claim 37, wherein the probe comprises a
5 nucleic acid sequence having at least 95% sequence identity to a nucleic acid comprising
a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth
in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a
subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a
sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth
10 in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or
a subsequence thereof; a sequence as set forth in SEQ ID NO:15, or a subsequence
thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence
as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ
ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a
15 subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence
thereof.

39. The nucleic acid probe of claim 38, wherein the probe comprises a
nucleic acid sequence having at least 98% sequence identity to a nucleic acid comprising
20 a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth
in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a
subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a
sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth
in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or
25 a subsequence thereof; a sequence as set forth in SEQ ID NO:15, or a subsequence
thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence
as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ
ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a
subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence
30 thereof.

40. An amplification primer sequence pair for amplifying a nucleic
acid encoding a polypeptide with a fluorescent activity, wherein the primer pair is capable
of amplifying a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a

subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

41. The nucleic acid probe of claim 40, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence.

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42. A method of amplifying a nucleic acid encoding a fluorescent polypeptide comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

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43. An expression cassette comprising a nucleic acid comprising
 (i) a nucleic acid comprising
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,
- 5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,
- 10 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,
- 15 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
- 20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
- 25 wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,
- (ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a
- 30

subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

5

44. A vector comprising a nucleic acid comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

10

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

15

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

20

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

25

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

30

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

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45. A cloning vehicle comprising a vector as set forth in claim 44, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

20

46. The cloning vehicle of claim 45, wherein the viral vector comprises an adenovirus vector, a retroviral vectors or an adeno-associated viral vector.

47. The cloning vehicle of claim 45 comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), a mammalian artificial chromosome (MAC)

25

48. A transformed cell comprising a vector, wherein the vector comprises

(i) a nucleic acid comprising
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

30

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

5 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

10 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

15 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

25 (ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set

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forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

49. A transformed cell comprising
- 5 (i) a nucleic acid comprising
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,
- 10 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID
- 15 NO:9 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,
- 20 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 70% sequence identity to SEQ ID
- 25 NO:19 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
- a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
- 30 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
- wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

50. The transformed cell of claim 48 or claim 49, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

51. A transgenic non-human animal comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

10 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a
 15 sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in
 20 SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

25

52. The transgenic non-human animal of claim 51, wherein the animal is a mouse.

53. The transgenic non-human animal of claim 51, wherein the animal
 30 is a rabbit.

54. A transgenic plant comprising
 (i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

10 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

15 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

20 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

25 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence

as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

55. The transgenic plant of claim 50, wherein the plant is an oilseed plant, a rapeseed plant, a soybean plant, a palm, a canola plant, a sunflower plant, a sesame plant, a peanut plant or a tobacco plant.

56. A transgenic seed comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

57. The transgenic seed of claim 56, wherein the seed is an oilseed, a rapeseed, a soybean seed, a palm kernel, a canola plant seed, a sunflower seed, a sesame seed, a peanut or a tobacco plant seed.

25

58. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

5 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

10 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

15 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

20 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a
 25 sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in
 30 SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

59. The antisense oligonucleotide of claim 58, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

5

60. An isolated or recombinant polypeptide comprising

(a) a polypeptide sequence comprising

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,

10 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and

15 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:10 over a region of at least about 100 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:12 over a region of at least about 100 residues,

20 an amino acid sequence having at least 65% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,

an amino acid sequence having at least 60% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

25 an amino acid sequence having at least 65% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,

an amino acid sequence having at least 60% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:22 over a region of at least about 100 residues,

30 an amino acid sequence having at least 85% sequence identity to SEQ ID NO:24 over a region of at least about 100 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:26 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; and,

(b) a polypeptide encoded by a nucleic acid comprising

(i) a nucleic acid comprising

5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

10 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

15 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

20 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

25 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

30 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a

sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

61. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises a fluorescent activity.

62. The isolated or recombinant polypeptide of claim 61, wherein the polypeptide comprises

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:2 over a region of at least about 200 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:4 over a region of at least about 200 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:6 over a region of at least about 200 residues, and

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:8 over a region of at least about 200 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:10 over a region of at least about 200 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:12 over a region of at least about 200 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:14 over a region of at least about 200 residues,

an amino acid sequence having at least 60% sequence identity to SEQ ID NO:16 over a region of at least about 200 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:18 over a region of at least about 200 residues,

an amino acid sequence having at least 60% sequence identity to SEQ ID NO:20 over a region of at least about 200 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:22 over a region of at least about 200 residues,

5 an amino acid sequence having at least 85% sequence identity to SEQ ID NO:24 over a region of at least about 200 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:26 over a region of at least about 200 residues.

10 63. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide sequence comprises

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:2 over a region of at least about 227 residues,

15 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:4 over a region of at least about 227 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:6 over a region of at least about 227 residues, and

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:8 over a region of at least about 227 residues,

20 an amino acid sequence having at least 65% sequence identity to SEQ ID NO:10 over a region of at least about 229 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:12 over a region of at least about 228 residues,

25 an amino acid sequence having at least 65% sequence identity to SEQ ID NO:14 over a region of at least about 225 residues,

an amino acid sequence having at least 60% sequence identity to SEQ ID NO:16 over a region of at least about 231 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:18 over a region of at least about 228 residues,

30 an amino acid sequence having at least 60% sequence identity to SEQ ID NO:20 over a region of at least about 253 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:22 over a region of at least about 261 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:24 over a region of at least about 261 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:26 over a region of at least about 260 residues.

5

64. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

an amino acid sequence having at least 75% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,

10 an amino acid sequence having at least 75% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,

an amino acid sequence having at least 75% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and

15 an amino acid sequence having at least 75% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:10 over a region of at least about 100 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:12 over a region of at least about 100 residues,

20 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

25 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues,

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:22 over a region of at least about 100 residues,

30 an amino acid sequence having at least 90% sequence identity to SEQ ID NO:24 over a region of at least about 100 residues,

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:26 over a region of at least about 100 residues.

65. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

an amino acid sequence having at least 80% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,

5 an amino acid sequence having at least 80% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,

an amino acid sequence having at least 80% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and

10 an amino acid sequence having at least 80% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,

an amino acid sequence having at least 80% sequence identity to SEQ ID NO:10 over a region of at least about 100 residues,

an amino acid sequence having at least 80% sequence identity to SEQ ID NO:12 over a region of at least about 100 residues,

15 an amino acid sequence having at least 75% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

20 an amino acid sequence having at least 75% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,

an amino acid sequence having at least 70% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues,

an amino acid sequence having at least 95% sequence identity to SEQ ID NO:22 over a region of at least about 100 residues,

25 an amino acid sequence having at least 95% sequence identity to SEQ ID NO:24 over a region of at least about 100 residues,

an amino acid sequence having at least 95% sequence identity to SEQ ID NO:26 over a region of at least about 100 residues.

30 66. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and

5 an amino acid sequence having at least 85% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,

an amino acid sequence having at least 85% sequence identity to SEQ ID NO:10 over a region of at least about 100 residues,

10 an amino acid sequence having at least 85% sequence identity to SEQ ID NO:12 over a region of at least about 100 residues,

an amino acid sequence having at least 80% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,

an amino acid sequence having at least 75% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

15 an amino acid sequence having at least 80% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,

an amino acid sequence having at least 75% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues,

20 an amino acid sequence having at least 98% sequence identity to SEQ ID NO:22 over a region of at least about 100 residues,

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:24 over a region of at least about 100 residues,

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:26 over a region of at least about 100 residues.

25

67. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,

30 an amino acid sequence having at least 90% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and

- an amino acid sequence having at least 90% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,
- an amino acid sequence having at least 90% sequence identity to SEQ ID NO:10 over a region of at least about 100 residues,
- 5 an amino acid sequence having at least 90% sequence identity to SEQ ID NO:12 over a region of at least about 100 residues,
- an amino acid sequence having at least 85% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,
- an amino acid sequence having at least 80% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,
- 10 an amino acid sequence having at least 85% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,
- an amino acid sequence having at least 80% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues,
- 15 an amino acid sequence having at least 99% sequence identity to SEQ ID NO:22 over a region of at least about 100 residues,
- an amino acid sequence having at least 99% sequence identity to SEQ ID NO:24 over a region of at least about 100 residues,
- an amino acid sequence having at least 99% sequence identity to SEQ ID NO:26 over a region of at least about 100 residues.
- 20

68. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

- an amino acid sequence having at least 95% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,
- 25 an amino acid sequence having at least 95% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,
- an amino acid sequence having at least 95% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and
- 30 an amino acid sequence having at least 95% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,
- an amino acid sequence having at least 95% sequence identity to SEQ ID NO:10 over a region of at least about 100 residues,

an amino acid sequence having at least 95% sequence identity to SEQ ID NO:12 over a region of at least about 100 residues,

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,

5 an amino acid sequence having at least 85% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,

10 an amino acid sequence having at least 85% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues.

69. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

15 an amino acid sequence having at least 98% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and

20 an amino acid sequence having at least 98% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:10 over a region of at least about 100 residues,

25 an amino acid sequence having at least 98% sequence identity to SEQ ID NO:12 over a region of at least about 100 residues,

an amino acid sequence having at least 95% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

30 an amino acid sequence having at least 95% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,

an amino acid sequence having at least 90% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues.

70. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:14 over a region of at least about 100 residues,

5 an amino acid sequence having at least 95% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:18 over a region of at least about 100 residues,

10 an amino acid sequence having at least 95% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues.

71. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises

15 an amino acid sequence having at least 98% sequence identity to SEQ ID NO:16 over a region of at least about 100 residues,

an amino acid sequence having at least 98% sequence identity to SEQ ID NO:20 over a region of at least about 100 residues.

72. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises an amino acid sequence as set forth in SEQ ID NO:2, an amino acid sequence as set forth in SEQ ID NO:4, an amino acid sequence as set forth in SEQ ID NO:6, an amino acid sequence as set forth in SEQ ID NO:8, an amino acid sequence as set forth in SEQ ID NO:10, an amino acid sequence as set forth in SEQ ID NO:12, an amino acid sequence as set forth in SEQ ID NO:14, an amino acid sequence as set forth in SEQ ID NO:16, a sequence as set forth in SEQ ID NO:18, or a subsequence thereof, a sequence as set forth in SEQ ID NO:20, or a subsequence thereof, a sequence as set forth in SEQ ID NO:22, or a subsequence thereof, a sequence as set forth in SEQ ID NO:24, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:26, or a subsequence thereof.

30

73. An isolated or recombinant polypeptide comprising the polypeptide as set forth in claim 60 and a heterologous signal sequence.

74. The isolated or recombinant polypeptide of claim 60, wherein the fluorescent activity comprises emission at 500 nm (green).

5 75. The isolated or recombinant polypeptide of claim 60, wherein the fluorescent activity comprises emission at 490 nm (cyan).

76. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises fluorescent activity after excitation at 485 nm (for green).

10 77. The isolated or recombinant polypeptide of claim 60, wherein the fluorescent activity comprises fluorescent activity after excitation at 460 nm (for cyan).

78. A protein preparation comprising a polypeptide as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

15

79. A homodimer comprising a polypeptide of the invention as set forth in claim 60.

20 80. A heterodimer comprising a polypeptide as set forth in claim 60 and a second domain.

81. The heterodimer of claim 80, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

25 82. The heterodimer of claim 80, wherein the second domain is an epitope.

83. The heterodimer of claim 80, wherein the second domain is a tag or a signal sequence.

30

84. An immobilized fluorescent polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 60 or claim 73.

85. The immobilized polypeptide of claim 84, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

5 86. An array comprising an immobilized polypeptide as set forth in claim 60 or claim 73.

87. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 29.

10

88. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 60 or to a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 29.

15 89. The isolated or recombinant antibody of claim 88, wherein the antibody is a monoclonal or a polyclonal antibody.

90. A hybridoma comprising an antibody as set forth in claim 89.

20 91. A method of isolating or identifying a fluorescent polypeptide comprising the steps of:

(a) providing an antibody as set forth in claim 88;

(b) providing a sample comprising polypeptides; and

(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a fluorescent protein.

92. A method of making an anti-fluorescent protein antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 29, or a polypeptide as set forth in claim 60, in an amount sufficient to generate a humoral immune response, thereby making an anti-fluorescent protein antibody.

93. A method of producing a recombinant polypeptide comprising the steps of:

(a) providing a nucleic acid operably linked to a promoter; wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 29; and

(b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

5

94. The method of claim 93, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

10

95. A method for identifying a polypeptide having a fluorescent activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid having a sequence as set forth in claim 1 or 29;

(b) providing an excitation source; and

15

(c) subjecting the polypeptide or a fragment or variant thereof of step (a) to an excitation energy provided by the excitation source of step (b) and detecting an emitted light by the polypeptide of step (a) thereby identifying a polypeptide having a fluorescent activity.

20

96. The method of claim 95, wherein the excitation occurs at a wavelength comprising the range from about 380 nm to about 510 nm.

97. The method of claim 96, wherein the emission occurs at a wavelength comprising the range from about 490 nm to about 510 nm.

25

98. A method for identifying an agent that changes a fluorescent polypeptide emission comprising the following steps:

(a) providing a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid having a sequence as set forth in claim 1 or 29;

30

(b) providing a test agent;

(c) contacting the polypeptide of step (a) with the agent of step (b) and measuring a fluorescent activity of the polypeptide of the invention, wherein a change in the fluorescent activity measured in the presence of the test agent compared to the activity

in the absence of the test agent provides a determination that the test agent changes the fluorescent activity.

5 99. The method of claim 98, wherein the test agent is a quencher of a fluorescent activity.

10 100. The method of claim 99, wherein a decrease in the amount of fluorescence with the test agent compared to the amount of fluorescence without the test agent identifies the test agent as a quencher of a fluorescent activity.

15 101. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a polypeptide sequence and a nucleic acid sequence, wherein the polypeptide comprises sequence as set forth in claim 60, or subsequence thereof, and the
nucleic acid comprises a sequence as set forth in claim 1 or 29, or a subsequence thereof.

20 102. The computer system of claim 101, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

 103. The computer system of claim 102, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

25 104. The computer system of claim 101, further comprising an identifier that identifies one or more features in the sequence.

30 105. A computer readable medium having stored thereon a sequence selected from the group consisting of a polypeptide sequence and a nucleic acid sequence, wherein the polypeptide comprises sequence as set forth in claim 60, or subsequence thereof, and the nucleic acid comprises a sequence as set forth in claim 1 or claim 29, or subsequence thereof.

 106. A method for identifying a feature in a sequence comprising the steps of:

(a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence and a nucleic acid sequence, wherein the polypeptide comprises a polypeptide sequence as set forth in claim 60, and the nucleic acid sequence comprises a sequence as set forth in claim 1 or claim 29.

(b) identifying one or more features in the sequence with the computer program.

107. A method for comparing a first sequence to a second sequence comprising the steps of:

(a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide comprises sequence as set forth in claim 60, or subsequence thereof, and the nucleic acid comprises a sequence as set forth in claim 1 or claim 29 or subsequence thereof; and

(b) determining differences between the first sequence and the second sequence with the computer program.

108. The method of claim 107, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

109. The method of claim 107, further comprising an identifier that identifies one or more features in a sequence.

25

110. The method of claim 107, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

111. A method for isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample comprising the steps of:

(a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide with a fluorescent activity, wherein the primer pair is capable of amplifying SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ

ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a fluorescent polypeptide from an environmental sample.

10

112. The method of claim 111, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, or a subsequence thereof.

113. A method for isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence or a subsequence comprising:

(i) a nucleic acid comprising
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

5 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

10 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

15 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample.

114. The method of claim 111 or claim 113, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

115. The method of claim 111, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

116. A method of generating a variant of a nucleic acid encoding a fluorescent protein comprising the steps of:

(a) providing a template nucleic acid comprising:

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID

NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID

NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID

NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID

NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID

NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID

NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID

NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID

NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

5 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

10 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a
 15 sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in
 20 SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

25

117. The method of claim 116, further comprising expressing the variant nucleic acid to generate a variant fluorescent polypeptide.

118. The method of claim 116, wherein the modifications, additions or
 30 deletions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site

saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

119. The method of claim 116, wherein the modifications, additions or
5 deletions are introduced by a method selected from the group consisting of
recombination, recursive sequence recombination, phosphothioate-modified DNA
mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point
mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical
mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection
10 mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble
mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

120. The method of claim 116, wherein the modifications, additions or
deletions are introduced by error-prone PCR.

15

121. The method of claim 116, wherein the modifications, additions or
deletions are introduced by shuffling.

122. The method of claim 116, wherein the modifications, additions or
20 deletions are introduced by oligonucleotide-directed mutagenesis.

123. The method of claim 116, wherein the modifications, additions or
deletions are introduced by assembly PCR.

25 124. The method of claim 116, wherein the modifications, additions or
deletions are introduced by sexual PCR mutagenesis.

125. The method of claim 116, wherein the modifications, additions or
deletions are introduced by *in vivo* mutagenesis.

30

126. The method of claim 116, wherein the modifications, additions or
deletions are introduced by cassette mutagenesis.

127. The method of claim 116, wherein the modifications, additions or deletions are introduced by recursive ensemble mutagenesis.

128. The method of claim 116, wherein the modifications, additions or deletions are introduced by exponential ensemble mutagenesis.

129. The method of claim 116, wherein the modifications, additions or deletions are introduced by site-specific mutagenesis.

130. The method of claim 116, wherein the modifications, additions or deletions are introduced by gene reassembly.

131. The method of claim 116, wherein the modifications, additions or deletions are introduced by synthetic ligation reassembly (SLR).

132. The method of claim 116, wherein the modifications, additions or deletions are introduced by gene site saturated mutagenesis (GSSM™).

133. The method of claim 116, wherein method is iteratively repeated until a fluorescent polypeptide having an altered or different activity or an altered or different stability from that of a fluorescent polypeptide encoded by the template nucleic acid is produced.

134. The method of claim 133, wherein the altered or different activity is a fluorescent activity under denaturing condition, wherein the polypeptide encoded by the template nucleic acid is not fluorescent under the denaturing condition.

135. The method of claim 133, wherein the altered or different activity is fluorescence under a high temperature, wherein the fluorescent polypeptide encoded by the template nucleic acid is not fluorescent under the high temperature.

136. The method of claim 116, wherein method is iteratively repeated until a fluorescent polypeptide coding sequence having an altered codon usage from that of the template nucleic acid is produced.

137. The method of claim 116, wherein method is iteratively repeated until a fluorescent polypeptide gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

5

138. A method for modifying codons in a nucleic acid encoding a fluorescent polypeptide to increase its expression in a host cell, the method comprising
(a) providing a nucleic acid encoding a fluorescent polypeptide comprising a sequence selected from the group consisting of:

10

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

15

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

20

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

25

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

30

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

5 (ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence
10 thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set
15 forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof, and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and
20 replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

25

139. A method for modifying codons in a nucleic acid encoding a fluorescent polypeptide, the method comprising

(a) providing a nucleic acid encoding a fluorescent polypeptide comprising a sequence as set forth in claim 1 or claim 29; and

30 (b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a fluorescent polypeptide.

140. A method for modifying codons in a nucleic acid encoding a fluorescent polypeptide to increase its expression in a host cell, the method comprising

(a) providing a nucleic acid encoding a fluorescent polypeptide comprising a sequence as set forth in claim 1 or claim 29; and

5 (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby
10 modifying the nucleic acid to increase its expression in a host cell.

141. A method for modifying a codon in a nucleic acid encoding a fluorescent polypeptide to decrease its expression in a host cell, the method comprising

(a) providing a nucleic acid encoding a fluorescent polypeptide comprising
15 a sequence as set forth in claim 1 or claim 29; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a
20 codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

142. The method of claim 140 or 141, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

25

143. A method for producing a library of nucleic acids encoding a plurality of modified fluorescent polypeptide active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the
30 method comprising:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO:1, a sequence as set forth in SEQ ID NO:3; a

sequence as set forth in SEQ ID NO:5, a sequence as set forth in SEQ ID NO:7, a sequence as set forth in SEQ ID NO:9, a sequence as set forth in SEQ ID NO:11, a sequence as set forth in SEQ ID NO:13, and a sequence as set forth in SEQ ID NO:15 or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof, and the nucleic acid encodes a fluorescent polypeptide active site; and

10 (b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified fluorescent polypeptide active sites.

144. The method of claim 143, comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system.

145. The method of claim 143, comprising mutagenizing the first nucleic acid of step (a) by a method comprising gene site-saturation mutagenesis (GSSM™).

25 146. The method of claim 143, comprising mutagenizing the first nucleic acid of step (a) by a method comprising a synthetic ligation reassembly (SLR).

147. The method of claim 143, further comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

148. The method of claim 143, further comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing
5 template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

10

149. A method for determining a functional fragment of a fluorescent polypeptide comprising the steps of:

(a) providing a fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a
15 sequence as set forth in claim 1 or claim 29; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a fluorescent activity, thereby determining a functional fragment of a fluorescent polypeptide.

20

150. The method of claim 149, wherein the fluorescence is measured by providing an excitation source set at the absorption wavelength of a fluorescent polypeptide and detecting an emission at the wavelength of the emission of a fluorescent polypeptide.

25

151. The method of claim 150, wherein a decrease in the amount of the fluorescence activity with the test agent as compared to the amount of fluorescence without the test agent identifies the test agent as a fluorescence quencher of the fluorescent activity.

30

152. A method for producing a chimeric polypeptide comprising the following steps:

(a) providing a fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 or claim 29; and

(b) providing a second polypeptide; and

(c) contacting the polypeptide of step (a) and the second polypeptide of step (b) under conditions wherein the fluorescent polypeptide can be fused with the second polypeptide, thereby producing a chimeric polypeptide.

5

153. The method of claim 152, wherein the chimeric polypeptide retains a fluorescent activity.

10

154. The method of claim 153, wherein the conditions under which the fluorescent polypeptide is fused with the second polypeptide comprise N-terminal fusion.

155. The method of claim 153, wherein the conditions under which the fluorescent polypeptide is fused with the second polypeptide comprise C-terminal fusion.

15

156. The method of claim 153, wherein the second polypeptide is capable of recognizing specific molecular structures.

157. The method of claim 156, wherein the second polypeptide is an antibody.

20

158. The method of claim 157, wherein the antibody is a polyclonal antibody.

25

159. The method of claim 157, wherein the antibody is a monoclonal antibody.

160. A method for producing a chimeric compound comprising the following steps:

30

(a) providing a first fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 or claim 29; and

(b) providing a second compound; and

(c) contacting the polypeptide of step (a) and the second compound of step (b) under conditions wherein the fluorescent polypeptide can be fused with the second compound, thereby producing a chimeric compound.

5 161. The method of claim 160, wherein the resulting chimeric compound retains a fluorescent activity.

162. The method of claim 161, wherein the fusion is N-terminal fusion.

10 163. The method of claim 160, wherein the fusion is C-terminal fusion.

164. A method for producing a nucleic acid with a fluorescent tag comprising of following steps:

15 (a) providing a first fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 or claim 29; and

(b) providing a nucleic acid; and

(c) contacting the polypeptide of step (a) and the nucleic acid of step (b) under conditions wherein the fluorescent polypeptide can covalently bind with the nucleic acid, thereby producing a nucleic acid with a fluorescent tag.

165. A method for using a polypeptide as a fluorescent marker comprising the following steps:

25 (a) providing a fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 or claim 29; or a chimeric polypeptide of claim 153, or a chimeric compound of claim 161, or a nucleic acid with a fluorescent tag of claim 164;

(b) providing an excitation source emitting light at the absorption wavelength of the fluorescent polypeptide; and

30 (c) detecting a fluorescent activity of the compound of step (a) at the emission wavelength of the fluorescent polypeptide.

166. The method of claim 165 further comprising the use as a fluorescent marker in receptor-ligand binding.

35

167. The method of claim 165, wherein the polypeptide is used as a fluorescent marker in immunoassays.

5 168. The method of claim 165, wherein the polypeptide is used as a fluorescent marker in single-step homogenous assays.

169. The method of claim 165, wherein the polypeptide is used as a fluorescent marker in multiple-step heterogeneous assays.

10

170. The method of claim 165, wherein the polypeptide is used as a fluorescent marker in enzyme assays.

171. The method of claim 165, wherein the polypeptide is used as a
15 fluorescent marker to measure protein-protein interactions.

172. The method of claim 165, wherein the polypeptide is used as a fluorescent marker in protein transport.

20 173. The method of claim 172, wherein the polypeptide is used as a fluorescent marker to monitor the subcellular targeting.

174. A method for using a fluorescent polypeptide in gene therapy comprising the following steps:

25 (a) obtaining from a patient a viable sample of primary cells of a particular cell type;

(b) inserting in the cells of step (a) a nucleic acid segment encoding a desired gene product;

(c) introducing in the cell of step (b) a vector comprising a nucleic acid of
30 the invention;

(d) identifying and isolating cells or cell lines that express the gene product of step (b);

(e) re-introducing the cells that express the gene product;

(f) removing from the patient an aliquot of tissue including cells resulting from step (d) and their progeny;

(g) determining the quantity of the cells resulting from the step (d) in the aliquot of step (f),

5 thereby the introduction of the vector comprising the nucleic acid of the invention in addition to the desired gene allows the identification of viable cells that contain and express the desired gene of step b.

175. A method of gene therapy comprising the following steps:

10 (a) providing a plurality of tissue cells;

(b) providing a retroviral vector encoding a desired gene product;

(c) providing a vector of the invention; and

(d) contacting the target cells of step (a) with the retroviral vectors of step (b) and a vector of the invention under conditions wherein the cells of step (a) are
15 transfected with the vectors of steps (b) and (c) allowing co-expression of the polypeptide of the invention, thereby allowing assessment of proportion of transfected cells and levels of expression.

176. The method of gene therapy as set forth in claim 175, wherein the
20 tissue cells further comprise cancerous or diseased cells

177. A method for diagnostic testing comprising the following steps:

(a) providing a vector of the invention as set forth in claim 44;

(b) placing the vector of step (a) under control of a promoter;

25 (c) providing an inducing agent to induce the promoter of step (b); and

(d) contacting the agent of step (c) with the promoter of step (b) under condition wherein the agent of step (c) induces the promoter of step (b), thereby causing the expression of a fluorescent polypeptide in cells, cell lines or tissues, wherein the cells, cell lines or tissue will become fluorescent in the presence of the inducing agent.

30

178. The method of claim 177, wherein the promoter is a viral promoter and the inducing agent is a corresponding virus.

179. The method of claim 177, wherein the promoter is a promoter of heat shock gene, and the inducing agent comprises various cellular stresses.

180. The method of claim 177, wherein the promoter is a promoter that
5 is sensitive to organismal responses.

181. The method of claim 170, wherein the organismal response is inflammation.

10 182. A method for assessing the effect of selected culture components and conditions on selected gene expression comprising the following steps:

(a) providing a cell comprising a nucleic acid as set forth in claim 1 or claim 29 operably linked to a regulatory sequence derived from a selected gene;

(b) incubating the cell of step (a) under selected culture conditions or in
15 the presence of selected components, wherein expressing the polypeptide of the invention; and

(c) detecting the presence and subcellular localization of fluorescent signal thereby assessing the effect of selected cultures components or condition on selected gene expression.

20

183. The method of claim 182, wherein selected culture conditions or components comprise salt concentration, pH, temperature, transacting regulatory substance, hormones, cell-cell contacts, ligands of cell surface or internal receptors.

25 184. A method for assessing a mutagenic potential of a test agent in a tissue culture or transgenic animal comprising the following steps:

(a) providing the nucleic acid of the invention as set forth in claim 1 or claim 29 operably linked to a transcriptional control element, wherein the transcription control element can be negatively regulated by a repressor;

30 (b) providing a repressor under control of a constitutively expressed gene;

(c) providing a test compound capable of interacting with a promoter of the constitutively expressed gene thereby turning it off; and

(d) contacting the test agent of step (c) with the repressor of step (b) under conditions wherein the test agent inactivates or turns off the gene expressing the repressor thereby causing the expression of the polypeptide of the invention.

5 185. The method of claim 184, wherein the mutagenicity of a test agent is assessed qualitatively by direct visualization of fluorescence in the cells.

186. The method of claim 184, wherein the mutagenicity of a test agent is assessed quantitatively by means of FACS of the cells.

10

187. A method for identifying a compound capable of changing expression of a target gene comprising of the following steps:

15 (a) providing a first nucleic acid having a sequence as set forth in claim 1 or claim 29 and expressing a first polypeptide, wherein the nucleic acid is operably linked to a promoter of a target gene in a cell;

20 (b) providing a second nucleic acid as set forth in claim 1 or 29, and expressing a second polypeptide, wherein the second nucleic acid is operably linked to a promoter of a constitutively expressed gene in a cell, wherein the first polypeptide emits a light at a wavelength different than the wavelength of the light emitted by the second polypeptide;

 (c) providing a compound affecting the expression of the target gene of step (a) by binding to the promoter of the target gene;

 (d) contacting the compound of step (c) with the cell of step (a);

 (e) expressing the first and second polypeptide, and

25 (f) detecting fluorescence of the first and second polypeptides,

 (i) wherein altered fluorescence of the first polypeptide and unchanged fluorescence of the second polypeptide demonstrates that the compound binds to the target gene promoter and has no non-specific or cytotoxic effects thereby not altering expression of the second polypeptide; or

30 (ii) wherein altered fluorescence of the first polypeptide and altered fluorescence of the second polypeptide demonstrates that the test drug has non-specific or cytotoxic effects thereby affecting the expression of the second polypeptide.

188. An isolated or recombinant nucleic acid comprising a sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197.

189. An isolated or recombinant nucleic acid comprising a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID

NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID
 NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID
 NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID
 NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID
 5 NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID
 NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID
 NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID
 NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID
 NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID
 10 NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID
 NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID
 NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID
 NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197.

15 190. An isolated or recombinant polypeptide comprising a sequence
 having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%,
 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%,
 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%,
 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID NO:2,
 20 SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID
 NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID
 NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID
 NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID
 NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID
 25 NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID
 NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID
 NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID
 NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID
 NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID
 30 NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID
 NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID
 NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID
 NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID
 NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154,

SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164,
 SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174,
 SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184,
 SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194,
 5 SEQ ID NO:196, SEQ ID NO:198.

191. An isolated or recombinant polypeptide having a sequence as set
 forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10,
 SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ
 10 ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID
 NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID
 NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID
 NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID
 NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID
 15 NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID
 NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID
 NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID
 NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID
 NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID
 20 NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID
 NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID
 NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152,
 SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162,
 SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172,
 25 SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182,
 SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192,
 SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198.

192. An isolated or recombinant nucleic acid having a sequence
 30 comprising any combination of segments whose overhangs as described in Figure 15 can
 anneal to each other.